

RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.**

Application Serial Number: 09/964,858C
Source: IFW/6
Date Processed by STIC: 6/15/06

ENTERED



IFW16

RAW SEQUENCE LISTING

DATE: 06/15/2006

PATENT APPLICATION: US/09/964,858C

TIME: 09:26:40

Input Set : A:\P07274US02_Sequence.txt

Output Set: N:\CRF4\06152006\I964858C.raw

3 <110> APPLICANT: HOSTETTER, Margaret K.
 4 DEVORE-CARTER, Denise
 6 <120> TITLE OF INVENTION: ANTIBODIES TO THE PROPEPTIDE OF CANDIDA ALBICANS
 8 <130> FILE REFERENCE: P07274US02/BAS
 10 <140> CURRENT APPLICATION NUMBER: US 09/964,858C
 11 <141> CURRENT FILING DATE: 2001-09-28
 13 <150> PRIOR APPLICATION NUMBER: US 60/237,082
 14 <151> PRIOR FILING DATE: 2000-09-28
 16 <160> NUMBER OF SEQ ID NOS: 13
 18 <170> SOFTWARE: PatentIn version 3.1
 20 <210> SEQ ID NO: 1
 21 <211> LENGTH: 1664
 22 <212> TYPE: PRT
 23 <213> ORGANISM: Candida albicans
 25 <400> SEQUENCE: 1
 27 Met Asn Ser Thr Pro Ser Lys Leu Leu Pro Ile Asp Lys His Ser His
 28 1 5 10 15
 31 Leu Gln Leu Gln Pro Gln Ser Ser Ser Ala Ser Ile Phe Asn Ser Pro
 32 20 25 30
 35 Thr Lys Pro Leu Asn Phe Pro Arg Thr Asn Ser Lys Pro Ser Leu Asp
 36 35 40 45
 39 Pro Asn Ser Ser Ser Asp Thr Tyr Thr Ser Glu Gln Asp Gln Glu Lys
 40 50 55 60
 43 Gly Lys Glu Glu Lys Lys Asp Thr Ala Phe Gln Thr Ser Phe Asp Arg
 44 65 70 75 80
 47 Asn Phe Asp Leu Asp Asn Ser Ile Asp Ile Gln Gln Thr Ile Gln His
 48 85 90 95
 51 Gln Gln Gln Gln Pro Gln Gln Gln Gln Gln Leu Ser Gln Thr Asp Asn
 52 100 105 110
 55 Asn Leu Ile Asp Glu Phe Ser Phe Gln Thr Pro Met Thr Ser Thr Leu
 56 115 120 125
 59 Asp Leu Thr Lys Gln Asn Pro Thr Val Asp Lys Val Asn Glu Asn His
 60 130 135 140
 63 Ala Pro Thr Tyr Ile Asn Thr Ser Pro Asn Lys Ser Ile Met Lys Lys
 64 145 150 155 160
 67 Ala Thr Pro Lys Ala Ser Pro Lys Lys Val Ala Phe Thr Val Thr Asn
 68 165 170 175
 71 Pro Glu Ile His Tyr Pro Asp Asn Arg Val Glu Glu Glu Asp Gln
 72 180 185 190
 75 Ser Gln Gln Lys Glu Asp Ser Val Glu Pro Pro Leu Ile Gln His Gln
 76 195 200 205
 79 Trp Lys Asp Pro Ser Gln Phe Asn Tyr Ser Asp Glu Asp Thr Asn Ala
 80 210 215 220

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83 Ser Val Pro Pro Thr Pro Pro Leu His Thr Thr Lys Pro Thr Phe Ala
84 225                230                235                240
87 Gln Leu Leu Asn Lys Asn Asn Glu Val Asn Ser Glu Pro Glu Ala Leu
88                245                250                255
91 Thr Asp Met Lys Leu Lys Arg Glu Asn Phe Ser Asn Leu Ser Leu Asp
92                260                265                270
95 Glu Lys Val Asn Leu Tyr Leu Ser Pro Thr Asn Asn Asn Asn Ser Lys
96                275                280                285
99 Asn Val Ser Asp Met Asp Ser His Leu Gln Asn Leu Gln Asp Ala Ser
100               290                295                300
103 Lys Asn Lys Thr Asn Glu Asn Ile His Asn Leu Ser Phe Ala Leu Lys
104 305                310                315                320
107 Ala Pro Lys Asn Asp Ile Glu Asn Pro Leu Asn Ser Leu Thr Asn Ala
108                325                330                335
111 Asp Ile Ser Leu Arg Ser Ser Gly Ser Ser Gln Ser Ser Leu Gln Ser
112                340                345                350
115 Leu Arg Asn Asp Asn Arg Val Leu Glu Ser Val Pro Gly Ser Pro Lys
116                355                360                365
119 Lys Val Asn Pro Gly Leu Ser Leu Asn Asp Gly Ile Lys Gly Phe Ser
120                370                375                380
123 Asp Glu Val Val Glu Ser Leu Leu Pro Arg Asp Leu Ser Arg Asp Lys
124 385                390                395                400
127 Leu Glu Thr Thr Lys Glu His Asp Ala Pro Glu His Asn Asn Glu Asn
128                405                410                415
131 Phe Ile Asp Ala Lys Ser Thr Asn Thr Asn Lys Gly Gln Leu Leu Val
132                420                425                430
135 Ser Ser Asp Asp His Leu Asp Ser Phe Asp Arg Ser Tyr Asn His Thr
136                435                440                445
139 Glu Gln Ser Ile Leu Asn Leu Leu Asn Ser Ala Ser Gln Ser Gln Ile
140                450                455                460
143 Ser Leu Asn Ala Leu Glu Lys Gln Arg Gln Thr Gln Glu Gln Glu Gln
144 465                470                475                480
147 Thr Gln Ala Ala Glu Pro Glu Glu Glu Thr Ser Phe Ser Asp Asn Ile
148                485                490                495
151 Lys Val Lys Gln Glu Pro Lys Ser Asn Leu Glu Phe Val Lys Val Thr
152                500                505                510
155 Ile Lys Lys Glu Pro Val Ser Ala Thr Glu Ile Lys Ala Pro Lys Arg
156                515                520                525
159 Glu Phe Ser Ser Arg Ile Leu Arg Ile Lys Asn Glu Asp Glu Ile Ala
160                530                535                540
163 Glu Pro Ala Asp Ile His Pro Lys Lys Glu Asn Glu Ala Asn Ser His
164 545                550                555                560
167 Val Glu Asp Thr Asp Ala Leu Leu Lys Lys Ala Leu Asn Asp Asp Glu
168                565                570                575
171 Glu Ser Asp Thr Thr Gln Asn Ser Thr Lys Met Ser Ile Arg Phe His
172                580                585                590
175 Ile Asp Ser Asp Trp Lys Leu Glu Asp Ser Asn Asp Gly Asp Arg Glu
176                595                600                605
179 Asp Asn Asp Asp Ile Ser Arg Phe Glu Lys Ser Asp Ile Leu Asn Asp

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180      610      615      620
183 Val Ser Gln Thr Ser Asp Ile Ile Gly Asp Lys Tyr Gly Asn Ser Ser
184 625      630      635      640
187 Ser Glu Ile Thr Thr Lys Thr Leu Ala Pro Pro Arg Ser Asp Asn Asn
188      645      650      655
191 Asp Lys Glu Asn Ser Lys Ser Leu Glu Asp Pro Ala Asn Asn Glu Ser
192      660      665      670
195 Leu Gln Gln Gln Leu Glu Val Pro His Thr Lys Glu Asp Asp Ser Ile
196      675      680      685
199 Leu Ala Asn Ser Ser Asn Ile Ala Pro Pro Glu Glu Leu Thr Leu Pro
200      690      695      700
203 Val Val Glu Ala Asn Asp Tyr Ser Ser Phe Asn Asp Val Thr Lys Thr
204 705      710      715      720
207 Phe Asp Ala Tyr Ser Ser Phe Glu Glu Ser Leu Ser Arg Glu His Glu
208      725      730      735
211 Thr Asp Ser Lys Pro Ile Asn Phe Ile Ser Ile Trp His Lys Gln Glu
212      740      745      750
215 Lys Gln Lys Lys His Gln Ile His Lys Val Pro Thr Lys Gln Ile Ile
216      755      760      765
219 Ala Ser Tyr Gln Gln Tyr Lys Asn Glu Gln Glu Ser Arg Val Thr Ser
220      770      775      780
223 Asp Lys Val Lys Ile Pro Asn Ala Ile Gln Phe Lys Lys Phe Lys Glu
224 785      790      795      800
227 Val Asn Val Met Ser Arg Arg Val Val Ser Pro Asp Met Asp Asp Leu
228      805      810      815
231 Asn Val Ser Gln Phe Leu Pro Glu Leu Ser Glu Asp Ser Gly Phe Lys
232      820      825      830
235 Asp Leu Asn Phe Ala Asn Tyr Ser Asn Asn Thr Asn Arg Pro Arg Ser
236      835      840      845
239 Phe Thr Pro Leu Ser Thr Lys Asn Val Leu Ser Asn Ile Asp Asn Asp
240      850      855      860
243 Pro Asn Val Val Glu Pro Pro Glu Pro Lys Ser Tyr Ala Glu Ile Arg
244 865      870      875      880
247 Asn Ala Arg Arg Leu Ser Ala Asn Lys Ala Ala Pro Asn Gln Ala Pro
248      885      890      895
251 Pro Leu Pro Pro Gln Arg Gln Pro Ser Ser Thr Arg Ser Asn Ser Asn
252      900      905      910
255 Lys Arg Val Ser Arg Phe Arg Val Pro Thr Phe Glu Ile Arg Arg Thr
256      915      920      925
259 Ser Ser Ala Leu Ala Pro Cys Asp Met Tyr Asn Asp Ile Phe Asp Asp
260      930      935      940
263 Phe Gly Ala Gly Ser Lys Pro Thr Ile Lys Ala Glu Gly Met Lys Thr
264 945      950      955      960
267 Leu Pro Ser Met Asp Lys Asp Asp Val Lys Arg Ile Leu Asn Ala Lys
268      965      970      975
271 Lys Gly Val Thr Gln Asp Glu Tyr Ile Asn Ala Lys Leu Val Asp Gln
272      980      985      990
275 Lys Pro Lys Lys Asn Ser Ile Val Thr Asp Pro Glu Asp Arg Tyr Glu
276      995      1000      1005

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279 Glu Leu Gln Gln Thr Ala Ser Ile His Asn Ala Thr Ile Asp Ser
280      1010      1015      1020
283 Ser Ile Tyr Gly Arg Pro Asp Ser Ile Ser Thr Asp Met Leu Pro
284      1025      1030      1035
287 Tyr Leu Ser Asp Glu Leu Lys Lys Pro Pro Thr Ala Leu Leu Ser
288      1040      1045      1050
291 Ala Asp Arg Leu Phe Met Glu Gln Glu Val His Pro Leu Arg Ser
292      1055      1060      1065
295 Asn Ser Val Leu Val His Pro Gly Ala Gly Ala Ala Thr Asn Ser
296      1070      1075      1080
299 Ser Met Leu Pro Glu Pro Asp Phe Glu Leu Ile Asn Ser Pro Ala
300      1085      1090      1095
303 Arg Asn Val Ser Asn Asn Ser Asp Asn Val Ala Ile Ser Gly Asn
304      1100      1105      1110
307 Ala Ser Thr Ile Ser Phe Asn Gln Leu Asp Met Asn Phe Asp Asp
308      1115      1120      1125
311 Gln Ala Thr Ile Gly Gln Lys Ile Gln Glu Gln Pro Ala Ser Lys
312      1130      1135      1140
315 Ser Ala Asn Thr Val Arg Gly Asp Asp Asp Gly Leu Ala Ser Ala
316      1145      1150      1155
319 Pro Glu Thr Pro Arg Thr Pro Thr Lys Lys Glu Ser Ile Ser Ser
320      1160      1165      1170
323 Lys Pro Ala Lys Leu Ser Ser Ala Ser Pro Arg Lys Ser Pro Ile
324      1175      1180      1185
327 Lys Ile Gly Ser Pro Val Arg Val Ile Lys Lys Asn Gly Ser Ile
328      1190      1195      1200
331 Ala Gly Ile Glu Pro Ile Pro Lys Ala Thr His Lys Pro Lys Lys
332      1205      1210      1215
335 Ser Phe Gln Gly Asn Glu Ile Ser Asn His Lys Val Arg Asp Gly
336      1220      1225      1230
339 Gly Ile Ser Pro Ser Ser Gly Ser Glu His Gln Gln His Asn Pro
340      1235      1240      1245
343 Ser Met Val Ser Val Pro Ser Gln Tyr Thr Asp Ala Thr Ser Thr
344      1250      1255      1260
347 Val Pro Asp Glu Asn Lys Asp Val Gln His Lys Pro Arg Glu Lys
348      1265      1270      1275
351 Gln Lys Gln Lys His His His Arg His His His His His His Lys
352      1280      1285      1290
355 Gln Lys Thr Asp Ile Pro Gly Val Val Asp Asp Glu Ile Pro Asp
356      1295      1300      1305
359 Val Gly Leu Gln Glu Arg Gly Lys Leu Phe Phe Arg Val Leu Gly
360      1310      1315      1320
363 Ile Lys Asn Ile Asn Leu Pro Asp Ile Asn Thr His Lys Gly Arg
364      1325      1330      1335
367 Phe Thr Leu Thr Leu Asp Asn Gly Val His Cys Val Thr Thr Pro
368      1340      1345      1350
371 Glu Tyr Asn Met Asp Asp His Asn Val Ala Ile Gly Lys Glu Phe
372      1355      1360      1365
375 Glu Leu Thr Val Ala Asp Ser Leu Glu Phe Ile Leu Thr Leu Lys

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376      1370      1375      1380
379 Ala Ser Tyr Glu Lys Pro Arg Gly Thr Leu Val Glu Val Thr Glu
380      1385      1390      1395
383 Lys Lys Val Val Lys Ser Arg Asn Arg Leu Ser Arg Leu Phe Gly
384      1400      1405      1410
387 Ser Lys Asp Ile Ile Thr Thr Thr Lys Phe Val Pro Thr Glu Val
388      1415      1420      1425
391 Lys Asp Thr Trp Ala Asn Lys Phe Ala Pro Asp Gly Ser Phe Ala
392      1430      1435      1440
395 Arg Cys Tyr Ile Asp Leu Gln Gln Phe Glu Asp Gln Ile Thr Gly
396      1445      1450      1455
399 Lys Ala Ser Gln Phe Asp Leu Asn Cys Phe Asn Glu Trp Glu Thr
400      1460      1465      1470
403 Met Ser Asn Gly Asn Gln Pro Met Lys Arg Gly Lys Pro Tyr Lys
404      1475      1480      1485
407 Ile Ala Gln Leu Glu Val Lys Met Leu Tyr Val Pro Arg Ser Asp
408      1490      1495      1500
411 Pro Arg Glu Ile Leu Pro Thr Ser Ile Arg Ser Ala Tyr Glu Ser
412      1505      1510      1515
415 Ile Asn Glu Leu Asn Asn Glu Gln Asn Asn Tyr Phe Glu Gly Tyr
416      1520      1525      1530
419 Leu His Gln Glu Gly Gly Asp Cys Pro Ile Phe Lys Lys Arg Phe
420      1535      1540      1545
423 Phe Lys Leu Met Gly Thr Ser Leu Leu Ala His Ser Glu Ile Ser
424      1550      1555      1560
427 His Lys Thr Arg Ala Lys Ile Asn Leu Ser Lys Val Val Asp Leu
428      1565      1570      1575
431 Ile Tyr Val Asp Lys Glu Asn Ile Asp Arg Ser Asn His Arg Asn
432      1580      1585      1590
435 Phe Ser Asp Val Leu Leu Leu Asp His Ala Phe Lys Ile Lys Phe
436      1595      1600      1605
439 Ala Asn Gly Glu Leu Ile Asp Phe Cys Ala Pro Asn Lys His Glu
440      1610      1615      1620
443 Met Lys Ile Trp Ile Gln Asn Leu Gln Glu Ile Ile Tyr Arg Asn
444      1625      1630      1635
447 Arg Phe Arg Arg Gln Pro Trp Val Asn Leu Met Leu Gln Gln Gln
448      1640      1645      1650
451 Gln Gln Gln Gln Gln Gln Gln Ser Ser Gln Gln
452      1655      1660

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455 <210> SEQ ID NO: 2

456 <211> LENGTH: 5194

457 <212> TYPE: DNA

458 <213> ORGANISM: Candida albicans

460 <400> SEQUENCE: 2

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461 cccaaaaaag ataaaataaa aacaaaacaa aacaaaagta ctaacaaatt attgaaactt      60
463 ttaattttta ataaagaatc agtagatcta ttgttaaaag aaatgaactc aactccaagt      120
465 aaattattac cgatagataa acattctcat ttacaattac agcctcaatc gtctctggca      180
467 tcaatattta attccccaac aaaaccattg aatttcccca gaacaaattc caagccgagt      240
469 ttgatccaa attcaagctc tgatacctac actagcgaac aagatcaaga gaaagggaaa      300

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RAW SEQUENCE LISTING ERROR SUMMARY DATE: 06/15/2006
PATENT APPLICATION: US/09/964,858C TIME: 09:26:41

Input Set : A:\P07274US02_Sequence.txt
Output Set: N:\CRF4\06152006\I964858C.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:13; Xaa Pos. 3

VERIFICATION SUMMARY

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Input Set : A:\P07274US02_Sequence.txt

Output Set: N:\CRF4\06152006\I964858C.raw

L:761 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13 after pos.:0